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SEQUENCE LISTING

<110> BAUMANN, PETER
CECH, THOMAS R.

<120> PROTECTION-OF-TELOMERE-1 (POT-1) PROTEIN AND ENCODING POLYNUCLEOTIDES

<130> 089491/0201

<140> 09/816,248
<141> 2001-03-26

<160> 45

<170> PatentIn Ver. 2.1

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        35                  40                  45

Cys Lys Val Ala Asp Pro Ser Ser Val Ala Lys Gly Gly Lys Leu Asn
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Thr Val Asn Val Val Phe Phe Ser Gln Asn Phe Glu Asp Leu Pro Ile
65                  70                  75                  80

Ile Gln Arg Val Gly Asp Ile Val Arg Val His Arg Ala Arg Leu Gln
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Leu Lys Val Val Asp Pro Ser Leu Tyr Leu Lys Ser Gln Lys Gly Thr
    50                  55                  60

Gly Asp Ala Ser Asp Tyr Ala Thr Leu Val Leu Tyr Ala Lys Arg Phe
65                  70                  75                  80

Glu Asp Leu Pro Ile Ile His Arg Ile Gly Asp Ile Ile Arg Val His
                85                  90                  95

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Asp Ala Thr Phe Pro Tyr Lys Thr Asn Gln Glu Arg Tyr Ile Cys Ser
        35                  40                  45

Leu Lys Ile Val Asp Pro Ser Leu Tyr Leu Lys Lys Glu Lys Gly Thr
    50                  55                  60

Gly Asp Asn Ser Asp Tyr Ala Thr Leu Val Leu Tyr Ala Lys Arg Phe
65                  70                  75                  80

Glu Asp Leu Pro Ile Ile His Arg Leu Gly Asp Ile Ile Arg Ile His
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Gly Asp Ala Ser Asp Tyr Ala Thr Leu Val Leu Tyr Ala Lys Arg Phe
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Glu Asp Leu Pro Ile Ile His Arg Ala Gly Asp Ile Ile Arg Val His
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Ser Gln Glu Leu Gln Lys Lys Asn Thr Ile Val Asn Leu Phe Gly Ile
         35                  40                  45

Val Lys Asp Phe Thr Pro Ser Arg Gln Ser Leu His Gly Thr Lys Asp
     50                  55                  60

Trp Val Thr Thr Val Tyr Leu Trp Asp Pro Thr Cys Asp Thr Ser Ser
 65                  70                  75                  80

Ile Gly Leu Gln Ile His Leu Phe Ser Lys Gln Gly Asn Asp Leu Pro
                 85                  90                  95

Val Ile Lys Gln Val Gly Gln Pro Leu Leu Leu His Gln Ile Thr Leu
            100                 105                 110

Arg Ser Tyr Arg Asp Arg Thr Gln Gly Leu Ser Lys Asp Gln Phe Arg
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Tyr Ala Leu Trp Pro Asp Phe Ser Ser Asn Ser Lys Asp Thr Leu Cys
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Pro Gln Pro Met Pro Arg Leu Met Lys Thr Gly Asp Lys Glu Glu Gln
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                165                 170                 175

Lys Asn Gly Glu Leu Leu Ser Thr Ser Ser Ala Arg Gln Asn Gln Thr
            180                 185                 190

Gly Leu Ser Tyr Pro Ser Val Ser Phe Ser Leu Leu Ser Gln Ile Thr
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Pro His Gln Arg Cys Ser Phe Tyr Ala Gln Val Ile Lys Thr Trp Tyr
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Ser Asp Lys Asn Phe Thr Leu Tyr Val Thr Asp Tyr Thr Glu Asn Glu
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Phe Tyr Cys Arg Asn Tyr Ile Lys Glu Gly Asp Tyr Val Val Met Lys
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His Gly Asp Ser Ala Lys Arg Tyr Asn Met Ser Ile Glu Lys Val Asp
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Val Gln Asn Cys Gln Asn Gly Ile Glu Ala Val Ile Glu Lys Leu Ser
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Leu Lys Leu Thr Thr Ile Ser Thr Ile Leu His Ala Pro Leu Gln Asn
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Ser Ser Lys Ile Gln Pro Cys Asn Leu Ala Asp His Pro Gln Met Thr
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Leu Gln Leu Lys Glu Arg Leu Phe Leu Ile Trp Gly Asn Leu Glu Glu
                485                 490                 495

Arg Ile Gln His His Ile Ser Lys Gly Glu Ser Pro Thr Leu Ala Ala
            500                 505                 510

Glu Asp Val Glu Thr Pro Trp Phe Asp Ile Tyr Val Lys Glu Tyr Ile
        515                 520                 525

Pro Val Ile Gly Asn Thr Lys Asp His Gln Ser Leu Thr Phe Leu Gln
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Ser Gln Glu Leu Gln Lys Lys Asn Thr Ile Val Asn Leu Phe Gly Ile
         35                  40                  45

Val Lys Asp Phe Thr Pro Ser Arg Gln Ser Leu His Gly Thr Lys Gly
     50                  55                  60

Met Leu Ala Tyr His Gly Gly Asn Tyr Thr Phe Tyr Phe Ser Ser Gln
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Glu Leu Ile Ile Met Phe Leu Asp Trp Val Thr Thr Val Tyr Leu Trp
                 85                  90                  95

Asp Pro Thr Cys Asp Thr Ser Ser Ile Gly Leu Gln Ile His Leu Phe
            100                 105                 110

Ser Lys Gln Gly Asn Asp Leu Pro Val Ile Lys Gln Val Gly Gln Pro
        115                 120                 125

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    130                 135                 140

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Ser Asn Ser Lys Asp Thr Leu Cys Pro Gln Pro Met Pro Arg Leu Met
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Lys Thr Gly Asp Lys Glu Glu Gln Phe Ala Leu Leu Leu Asn Lys Ile
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Trp Asp Glu Gln Thr Asn Lys His Lys Asn Gly Glu Leu Leu Ser Thr
        195                 200                 205

Ser Ser Ala Arg Gln Asn Gln Thr Gly Leu Ser Tyr Pro Ser Val Ser
    210                 215                 220

Phe Ser Leu Leu Ser Gln Ile Thr Pro His Gln Arg Cys Ser Phe Tyr
225                 230                 235                 240

Ala Gln Val Ile Lys Thr Trp Tyr Ser Asp Lys Asn Phe Thr Leu Tyr
                245                 250                 255
```

```
Val Thr Asp Tyr Thr Glu Asn Glu Leu Phe Phe Pro Met Ser Pro Tyr
            260                 265                 270

Thr Ser Ser Ser Arg Trp Arg Gly Pro Phe Gly Arg Phe Ser Ile Arg
        275                 280                 285

Cys Ile Leu Trp Asp Glu His Asp Phe Tyr Cys Arg Asn Tyr Ile Lys
    290                 295                 300

Glu Gly Asp Tyr Val Val Met Lys Asn Val Arg Thr Lys Ile Asp His
305                 310                 315                 320

Leu Gly Tyr Leu Glu Cys Ile Leu His Gly Asp Ser Ala Lys Arg Tyr
                325                 330                 335

Asn Met Ser Ile Glu Lys Val Asp Ser Glu Glu Pro Glu Leu Asn Glu
            340                 345                 350

Ile Lys Ser Arg Lys Arg Leu Tyr Val Gln Asn Cys Gln Asn Gly Ile
        355                 360                 365

Glu Ala Val Ile Glu Lys Leu Ser Gln Ser Gln Gln Ser Glu Asn Pro
    370                 375                 380

Phe Ile Ala His Glu Leu Lys Gln Thr Ser Val Asn Glu Ile Thr Ala
385                 390                 395                 400

His Val Ile Asn Glu Pro Ala Ser Leu Lys Leu Thr Thr Ile Ser Thr
                405                 410                 415

Ile Leu His Ala Pro Leu Gln Asn Leu Leu Lys Pro Arg Lys His Arg
            420                 425                 430

Leu Arg Val Gln Val Val Asp Phe Trp Pro Lys Ser Leu Thr Gln Phe
        435                 440                 445

Ala Val Leu Ser Gln Pro Pro Ser Ser Tyr Val Trp Met Phe Ala Leu
    450                 455                 460

Leu Val Arg Asp Val Ser Asn Val Thr Leu Pro Val Ile Phe Phe Asp
465                 470                 475                 480

Ser Asp Ala Ala Glu Leu Ile Asn Ser Ser Lys Ile Gln Pro Cys Asn
                485                 490                 495

Leu Ala Asp His Pro Gln Met Thr Leu Gln Leu Lys Glu Arg Leu Phe
            500                 505                 510

Leu Ile Trp Gly Asn Leu Glu Glu Arg Ile Gln His His Ile Ser Lys
        515                 520                 525

Gly Glu Ser Pro Thr Leu Ala Ala Glu Asp Val Glu Thr Pro Trp Phe
    530                 535                 540

Asp Ile Tyr Val Lys Glu Tyr Ile Pro Val Ile Gly Asn Thr Lys Asp
545                 550                 555                 560
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His Gln Ser Leu Thr Phe Leu Gln Lys Arg Trp Arg Gly Phe Gly Thr
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Lys Ile Val
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<210> 12
<211> 1905
<212> DNA
<213> Homo sapiens

<400> 12

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<210> 13
<211> 634
<212> PRT
<213> Homo sapiens

<400> 13

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Met Ser Leu Val Pro Ala Thr Asn Tyr Ile Tyr Thr Pro Leu Asn Gln
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Leu Lys Gly Gly Thr Ile Val Asn Val Tyr Gly Val Val Lys Phe Phe
             20                  25                  30
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```
Lys Pro Pro Tyr Leu Ser Lys Gly Thr Asp Tyr Cys Ser Val Val Thr
          35                  40                  45

Ile Val Asp Gln Thr Asn Val Lys Leu Thr Cys Leu Leu Phe Ser Gly
     50                  55                  60

Asn Tyr Glu Ala Leu Pro Ile Ile Tyr Lys Asn Gly Asp Ile Val Arg
 65                  70                  75                  80

Phe His Arg Leu Lys Ile Gln Val Tyr Lys Lys Glu Thr Gln Gly Ile
                 85                  90                  95

Thr Ser Ser Gly Phe Ala Ser Leu Thr Phe Glu Gly Thr Leu Gly Ala
            100                 105                 110

Pro Ile Ile Pro Arg Thr Ser Ser Lys Tyr Phe Asn Phe Thr Thr Glu
        115                 120                 125

Asp His Lys Met Val Glu Ala Leu Arg Val Trp Ala Ser Thr His Met
    130                 135                 140

Ser Pro Ser Trp Thr Leu Leu Lys Leu Cys Asp Val Gln Pro Met Gln
145                 150                 155                 160

Tyr Phe Asp Leu Thr Cys Gln Leu Leu Gly Lys Ala Glu Val Asp Gly
                165                 170                 175

Ala Ser Phe Leu Leu Lys Val Trp Asp Gly Thr Arg Thr Pro Phe Pro
            180                 185                 190

Ser Trp Arg Val Leu Ile Gln Asp Leu Val Leu Glu Gly Asp Leu Ser
        195                 200                 205

His Ile His Arg Leu Gln Asn Leu Thr Ile Asp Ile Leu Val Tyr Asp
    210                 215                 220

Asn His Val His Val Ala Arg Ser Leu Lys Val Gly Ser Phe Leu Arg
225                 230                 235                 240

Ile Tyr Ser Leu His Thr Lys Leu Gln Ser Met Asn Ser Glu Asn Gln
                245                 250                 255

Thr Met Leu Ser Leu Glu Phe His Leu His Gly Gly Thr Ser Tyr Gly
            260                 265                 270

Arg Gly Ile Arg Val Leu Pro Glu Ser Asn Ser Asp Val Asp Gln Leu
        275                 280                 285

Lys Lys Asp Leu Glu Ser Ala Asn Leu Thr Ala Asn Gln His Ser Asp
    290                 295                 300

Val Ile Cys Gln Ser Glu Pro Asp Asp Ser Phe Pro Ser Ser Gly Ser
305                 310                 315                 320

Val Ser Leu Tyr Glu Val Glu Arg Cys Gln Gln Leu Ser Ala Thr Ile
                325                 330                 335
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Leu Thr Asp His Gln Tyr Leu Glu Arg Thr Pro Leu Cys Ala Ile Leu
            340                 345                 350

Lys Gln Lys Ala Pro Gln Gln Tyr Arg Ile Arg Ala Lys Leu Arg Ser
        355                 360                 365

Tyr Lys Pro Arg Arg Leu Phe Gln Ser Val Lys Leu His Cys Pro Lys
    370                 375                 380

Cys His Leu Leu Gln Glu Val Pro His Glu Gly Asp Leu Asp Ile Ile
385                 390                 395                 400

Phe Gln Asp Gly Ala Thr Lys Thr Pro Val Val Lys Leu Gln Asn Thr
                405                 410                 415

Ser Leu Tyr Asp Ser Lys Ile Trp Thr Thr Lys Asn Gln Lys Gly Arg
            420                 425                 430

Lys Val Ala Val His Phe Val Lys Asn Asn Gly Ile Leu Pro Leu Ser
        435                 440                 445

Asn Glu Cys Leu Leu Leu Ile Glu Gly Gly Thr Leu Ser Glu Ile Cys
    450                 455                 460

Lys Leu Ser Asn Lys Phe Asn Ser Val Ile Pro Val Arg Ser Gly His
465                 470                 475                 480

Glu Asp Leu Glu Leu Leu Asp Leu Ser Ala Pro Phe Leu Ile Gln Gly
                485                 490                 495

Thr Ile His His Tyr Gly Cys Lys Gln Cys Ser Ser Leu Arg Ser Ile
            500                 505                 510

Gln Asn Leu Asn Ser Leu Val Asp Lys Thr Ser Trp Ile Pro Ser Ser
        515                 520                 525

Val Ala Glu Ala Leu Gly Ile Val Pro Leu Gln Tyr Val Phe Val Met
    530                 535                 540

Thr Phe Thr Leu Asp Asp Gly Thr Gly Val Leu Glu Ala Tyr Leu Met
545                 550                 555                 560

Asp Ser Asp Lys Phe Phe Gln Ile Pro Ala Ser Glu Val Leu Met Asp
                565                 570                 575

Asp Asp Leu Gln Lys Ser Val Asp Met Ile Met Asp Met Phe Cys Pro
            580                 585                 590

Pro Gly Ile Lys Ile Asp Ala Tyr Pro Trp Leu Glu Cys Phe Ile Lys
        595                 600                 605

Ser Tyr Asn Val Thr Asn Gly Thr Asp Asn Gln Ile Cys Tyr Gln Ile
    610                 615                 620

Phe Asp Thr Thr Val Ala Glu Asp Val Ile
625                 630
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<211> 1298
<212> DNA
<213> Homo sapiens

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<210> 15
<211> 340
<212> PRT
<213> Homo sapiens

<400> 15
Met Ser Leu Val Pro Ala Thr Asn Tyr Ile Tyr Thr Pro Leu Asn Gln
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Leu Lys Gly Gly Thr Ile Val Asn Val Tyr Gly Val Val Lys Phe Phe
20 25 30

Lys Pro Pro Tyr Leu Ser Lys Gly Thr Asp Tyr Cys Ser Val Val Thr
35 40 45

Ile Val Asp Gln Thr Asn Val Lys Leu Thr Cys Leu Leu Phe Ser Gly
50 55 60

Asn Tyr Glu Ala Leu Pro Ile Ile Tyr Lys Asn Gly Asp Ile Val Arg
65 70 75 80

Phe His Arg Leu Lys Ile Gln Val Tyr Lys Lys Glu Thr Gln Gly Ile
85 90 95

Thr Ser Ser Gly Phe Ala Ser Leu Thr Phe Glu Gly Thr Leu Gly Ala
100 105 110

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Pro Ile Ile Pro Arg Thr Ser Ser Lys Tyr Phe Asn Phe Thr Thr Glu
        115                 120                 125

Asp His Lys Met Val Glu Ala Leu Arg Val Trp Ala Ser Thr His Met
    130                 135                 140

Ser Pro Ser Trp Thr Leu Leu Lys Leu Cys Asp Val Gln Pro Met Gln
145                 150                 155                 160

Tyr Phe Asp Leu Thr Cys Gln Leu Leu Gly Lys Ala Glu Val Asp Gly
                165                 170                 175

Ala Ser Phe Leu Leu Lys Val Trp Asp Gly Thr Arg Thr Pro Phe Pro
            180                 185                 190

Ser Trp Arg Val Leu Ile Gln Asp Leu Val Leu Glu Gly Asp Leu Ser
        195                 200                 205

His Ile His Arg Leu Gln Asn Leu Thr Ile Asp Ile Leu Val Tyr Asp
    210                 215                 220

Asn His Val His Val Ala Arg Ser Leu Lys Val Gly Ser Phe Leu Arg
225                 230                 235                 240

Ile Tyr Ser Leu His Thr Lys Leu Gln Ser Met Asn Ser Glu Asn Gln
                245                 250                 255

Thr Met Leu Ser Leu Glu Phe His Leu His Gly Gly Thr Ser Tyr Gly
            260                 265                 270

Arg Gly Ile Arg Val Leu Pro Glu Ser Asn Ser Asp Val Asp Gln Leu
        275                 280                 285

Lys Lys Asp Leu Glu Ser Ala Asn Leu Thr Ala Asn Gln His Ser Asp
    290                 295                 300

Val Ile Cys Gln Ser Glu Pro Asp Asp Ser Phe Pro Asn Gly Val Ser
305                 310                 315                 320

Leu Arg Pro Pro Gly Trp Ser Ser Val Ala Arg Ser Arg Leu Ile Ala
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Ala Ser Thr Ser
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<211> 1816
<212> DNA
<213> Homo sapiens

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<210> 17
<211> 518
<212> PRT
<213> Homo sapiens

<400> 17

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Met Ser Leu Val Pro Ala Thr Asn Tyr Ile Tyr Thr Pro Leu Asn Gln
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Leu Lys Gly Gly Thr Ile Val Asn Val Tyr Gly Val Val Lys Phe Phe
             20                  25                  30

Lys Pro Pro Tyr Leu Ser Lys Gly Thr Asp Tyr Cys Ser Val Val Thr
         35                  40                  45

Ile Val Asp Gln Thr Asn Val Lys Leu Thr Cys Leu Leu Phe Ser Gly
     50                  55                  60

Asn Tyr Glu Ala Leu Pro Ile Ile Tyr Lys Asn Gly Asp Ile Val Arg
 65                  70                  75                  80

Phe His Arg Leu Lys Ile Gln Val Tyr Lys Lys Glu Thr Gln Gly Ile
                 85                  90                  95

Thr Ser Ser Gly Phe Ala Ser Leu Thr Phe Glu Gly Thr Leu Gly Ala
            100                 105                 110

Pro Ile Ile Pro Arg Thr Ser Ser Lys Tyr Phe Asn Phe Thr Thr Glu
        115                 120                 125
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Asp His Lys Met Val Glu Ala Leu Arg Val Trp Ala Ser Thr His Met
    130                 135                 140

Ser Pro Ser Trp Thr Leu Leu Lys Leu Cys Asp Val Gln Pro Met Gln
145                 150                 155                 160

Tyr Phe Asp Leu Thr Cys Gln Leu Leu Gly Lys Ala Glu Val Asp Gly
                165                 170                 175

Ala Ser Phe Leu Leu Lys Val Trp Asp Gly Thr Arg Thr Pro Phe Pro
            180                 185                 190

Ser Trp Arg Val Leu Ile Gln Asp Leu Val Leu Glu Gly Asp Leu Ser
        195                 200                 205

His Ile His Arg Leu Gln Asn Leu Thr Ile Asp Ile Leu Val Tyr Asp
    210                 215                 220

Asn His Val His Val Ala Arg Ser Leu Lys Val Gly Ser Phe Leu Arg
225                 230                 235                 240

Ile Tyr Ser Leu His Thr Lys Leu Gln Ser Met Asn Ser Glu Asn Gln
                245                 250                 255

Thr Met Leu Ser Leu Glu Phe His Leu His Gly Gly Thr Ser Tyr Gly
            260                 265                 270

Arg Gly Ile Arg Val Leu Pro Glu Ser Asn Ser Asp Val Asp Gln Leu
        275                 280                 285

Lys Lys Asp Leu Glu Ser Ala Asn Leu Thr Ala Asn Gln His Ser Asp
    290                 295                 300

Val Ile Cys Gln Ser Glu Pro Asp Asp Ser Phe Pro Ser Ser Gly Ser
305                 310                 315                 320

Val Ser Leu Tyr Glu Val Glu Arg Cys Gln Gln Leu Ser Ala Thr Ile
                325                 330                 335

Leu Thr Asp His Gln Tyr Leu Glu Arg Thr Pro Leu Cys Ala Ile Leu
            340                 345                 350

Lys Gln Lys Ala Pro Gln Gln Tyr Arg Ile Arg Ala Lys Leu Arg Ser
        355                 360                 365

Tyr Lys Pro Arg Arg Leu Phe Gln Ser Val Lys Leu His Cys Pro Lys
    370                 375                 380

Cys His Leu Leu Gln Glu Val Pro His Glu Gly Asp Leu Asp Ile Ile
385                 390                 395                 400

Phe Gln Asp Gly Ala Thr Lys Thr Pro Asp Val Lys Leu Gln Asn Thr
                405                 410                 415

Ser Leu Tyr Asp Ser Lys Ile Trp Thr Thr Lys Asn Gln Lys Gly Arg
            420                 425                 430
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Lys Val Ala Val His Phe Val Lys Asn Asn Gly Ile Leu Pro Leu Ser
435 440 445

Asn Glu Cys Leu Leu Leu Ile Glu Gly Gly Thr Leu Ser Glu Ile Cys
450 455 460

Lys Leu Ser Asn Lys Phe Asn Ser Val Ile Pro Val Arg Ser Gly His
465 470 475 480

Glu Asp Leu Glu Leu Leu Asp Leu Ser Ala Pro Phe Leu Ile Gln Gly
485 490 495

Thr Ile His His Tyr Gly Thr Gly Tyr Cys Thr Pro Pro Ile Cys Val
500 505 510

Cys Tyr Asp Leu Tyr Thr
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<210> 18
<211> 27377
<212> DNA
<213> Homo sapiens

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<223> Description of Artificial Sequence: hPot1p-binding oligonucleotide

<400> 38
ttagggttag ggttagggtt agggttaggg 30

<210> 39
<211> 45
<212> PRT
<213> Schizosaccharomyces pombe

<400> 39
Met Gly Glu Asp Val Ile Asp Ser Leu Gln Leu Asn Glu Leu Leu Asn
1 5 10 15

Ala Gly Glu Tyr Lys Ile Gly Val Arg Tyr Gln Trp Ile Tyr Ile Cys
20 25 30

Phe Ala Asn Asn Glu Lys Gly Thr Tyr Ile Ser Val His
35 40 45

<210> 40
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C-strand binding specificity of SpPot1p

<400> 40
cgtaaccgta accctgtaac ctgtaacctg taaccgtgta acc 43

<210> 41
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PBoli109 oligonucleotide

<400> 41
ccgtaagcat ttcattattg gaattcgagc tcgttttcga 40

<210> 42
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PBoli164T oligonucleotide

<400> 42
ttcagatgtt atctgtcaat cagaacctg 29

<210> 43
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PBoli194B oligonucleotide

<400> 43
gaacactgtt tacatccata gtgatgtatt gttcc 35

<210> 44
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 44
tgaaggtcgg agtcaacgga tttggt 26

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45
catgtgggcc atgaggtcca ccac 24